

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 17:42:21 ; Search time 9796 Seconds
(without alignments)
11605.633 Million cell updates/sec

Title: US-09-623-596-1_COPY_1_2623
Perfect score: 2623
Sequence: 1 aagcttcggggaggggcgcg.....tgatgacctcgcatttggtg 2623

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2612	99.6	5348	1	AB041009	AB041009 Corynebac
c	2	2511.6	95.8	337200	1	AP005280	AP005280 Corynebac
c	3	2511.6	95.8	349980	6	AX127150	AX127150 Sequence
	4	2016	76.9	2242	6	AX771905	AX771905 Sequence
	5	1758.6	67.0	1953	6	AX122456	AX122456 Sequence
	6	1758.6	67.0	1953	6	BD164573	BD164573 Novel pol
c	7	1208.6	46.1	306650	1	AP005221	AP005221 Corynebac
c	8	604.4	23.0	348408	1	BX248358	BX248358 Corynebac
	9	595	22.7	795	6	AX122457	AX122457 Sequence
	10	595	22.7	795	6	BD164574	BD164574 Novel pol
c	11	399	15.2	38859	1	MLCB268	AL022602 Mycobacte
	12	399	15.2	348450	1	MLEPRTN4	AL583920 Mycobacte
c	13	390	14.9	15776	1	AE007069	AE007069 Mycobacte
c	14	390	14.9	37586	6	AX191745	AX191745 Sequence
c	15	390	14.9	306050	1	BX248341	BX248341 Mycobacte
c	16	390	14.9	348247	15	BX842579	Bx842579 Mycobacte
	17	155	5.9	11803	1	AE014760	AE014760 Bifidobac
	18	155	5.9	349980	6	AX492786	AX492786 Sequence
	19	155	5.9	349980	6	AX553953	AX553953 Sequence
	20	116.2	4.4	2951	1	AF123319	AF123319 Streptomy
c	21	116.2	4.4	321250	1	SC0939111	AL939111 Streptomy
	22	101.6	3.9	299925	1	AP005045	AP005045 Streptomy
c	23	92.2	3.5	301205	1	AE017218	AE017218 Geobacter
	24	89.6	3.4	249150	1	AP005332	AP005332 Vibrio vu
c	25	89.6	3.4	301442	1	AE016798	AE016798 Vibrio vu
c	26	84	3.2	208524	1	AE016925	AE016925 Chromobac
c	27	83.8	3.2	10423	1	AE007547	AE007547 Clostridi
	28	82.6	3.1	301995	1	AE016779	AE016779 Pseudomon
	29	81.8	3.1	7983	1	AE013142	AE013142 Thermoana
c	30	81	3.1	11975	1	AE013120	AE013120 Thermoana
	31	79.8	3.0	2154	1	AY142812	AY142812 Heliobaci
	32	78.8	3.0	192000	1	AE001438	AE001438 Clostridi
c	33	78.2	3.0	300950	1	AP001516	AP001516 Bacillus

called fts I

ATCC 13032 genome

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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 17:41:51 ; Search time 949 Seconds
(without alignments)
11741.858 Million cell updates/sec

Title: US-09-623-596-1_COPY_1_2623
Perfect score: 2623
Sequence: 1 aagcttcggggaggggcgcg.....tgatgatcctcgatttggtg 2623

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
c	1	2623	100.0	5347	2 AAZ09633	Aaz09633 B. lactof
	2	2511.6	95.8	349980	5 AAH68531	Aah68531 C glutami
	3	2016	76.9	2242	9 ADD13716	Add13716 C. glutam
	4	1758.6	67.0	1953	5 AAH67337	Aah67337 C glutami
	5	596.6	22.7	1827	7 ACA29976	Aca29976 Prokaryot
	6	595	22.7	795	5 AAH67338	Aah67338 C glutami
	7	403.2	15.4	1989	7 ACA38015	Aca38015 Prokaryot

APPL.

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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 17:45:31 ; Search time 5965 Seconds
(without alignments)
13131.349 Million cell updates/sec

Title: US-09-623-596-1_COPY_1_2623
Perfect score: 2623
Sequence: 1 aagcttcggggaggggcgcg.....tgatgatcctcgatttggtg 2623

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						
No.	Score	Match	Length	DB	ID	Description	
	1	98.6	3.8	507	28	BH740525	BH740525 cpbav0010
c	2	85.8	3.3	549	28	BH740502	BH740502 cpbav0008
	3	58.4	2.2	1133	28	BZ565848	BZ565848 pacs2-164
	4	57.4	2.2	1297	28	BZ565839	BZ565839 pacs2-164
	5	56.8	2.2	1138	28	BZ568217	BZ568217 pacs2-164
	6	54.2	2.1	713	14	CF887190	CF887190 UI-CF-FN0
	7	54	2.1	1344	28	BH770683	BH770683 LLMGtag43
	8	49.4	1.9	307	10	BF065979	BF065979 HV_CEB001
c	9	48.6	1.9	962	28	BZ554173	BZ554173 pacs1-60_
	10	44.8	1.7	1201	13	BX381961	BX381961 BX381961
c	11	44.6	1.7	1201	13	BX356664	BX356664 BX356664
c	12	42.2	1.6	1201	13	BX381961	BX381961 BX381961
c	13	42.2	1.6	1201	13	BX440707	BX440707 BX440707
	14	41.6	1.6	819	28	CC114410	CC114410 NDL.70I5.
c	15	41.6	1.6	910	29	CNS0060N	AL065629 Drosophil
	16	41.4	1.6	600	10	BF006977	BF006977 1163138 A
c	17	41.4	1.6	609	28	CC063491	CC063491 fgma001d0
	18	41	1.6	747	12	BI890692	BI890692 ZF637-2-0
c	19	41	1.6	925	29	CNS0091P	AL053013 Drosophil
	20	40.4	1.5	1856	9	AL696950	AL696950 AL696950
c	21	40.2	1.5	712	13	BX416727	BX416727 BX416727
	22	40.2	1.5	1201	13	BX360624	BX360624 BX360624
c	23	40	1.5	1101	29	CNS014Y2	AL104756 Drosophil
c	24	39.6	1.5	1071	29	CNS00EMY	AL069395 Drosophil
	25	39.6	1.5	1108	13	BX382084	BX382084 BX382084
	26	39.2	1.5	812	29	CNS0104Q	AL153067 Anopheles
	27	39.2	1.5	839	29	CNS004NB	AL054280 Drosophil
	28	39	1.5	462	9	AL822466	AL822466 AL822466
	29	39	1.5	514	14	CA409494	CA409494 1031_F -P
	30	39	1.5	517	28	AZ342386	AZ342386 1M0075K24
	31	39	1.5	798	13	CA103884	CA103884 SCEZHR108
	32	39	1.5	914	11	CNS09N4Y	BX066062 Single re
	33	39	1.5	917	11	CNS09M71	BX064841 Single re
c	34	38.8	1.5	1201	13	BX376097	BX376097 BX376097
	35	38.6	1.5	234	28	BH643123	BH643123 1008052B0
c	36	38.4	1.5	309	9	AI213021	AI213021 y6e10a1.f
c	37	38.4	1.5	316	9	AA784731	AA784731 g2a02a1.f
c	38	38.4	1.5	513	14	CD211465	CD211465 HS1_60_A0
	39	38.4	1.5	709	9	AJ558868	AJ558868 AJ558868
	40	38.2	1.5	656	14	CA186387	CA186387 SCSGST311
	41	38.2	1.5	710	14	CA216650	CA216650 SCCCST3C1
c	42	38	1.4	480	13	BQ363085	BQ363085 QV0-ST023
	43	38	1.4	515	13	BX424977	BX424977 BX424977
	44	38	1.4	711	13	BU023819	BU023819 QHF12P18.
	45	38	1.4	821	14	CF150908	CF150908 AGENCOURT

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2004, 11:23:25 ; Search time 5372.72 Seconds
(without alignments)
4687.072 Million cell updates/sec

Title: US-09-623-596-2
Perfect score: 2918
Sequence: 1 MVTRIALVIAGVLIIRLGWV.....TRNTGLPSRVLHPLMILDLL 581

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09623596/runat_09092004_094653_11700/app_query.fasta_1
.1486

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09623596 @CGN_1_1_8050 @runat_09092004_094653_11700 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
	1	2898	99.3	5348	1	AB041009	AB041009 Corynebac
	2	2848	97.6	1953	6	AX122456	AX122456 Sequence
	3	2848	97.6	1953	6	BD164573	BD164573 Novel pol
	4	2848	97.6	2242	6	AX771905	AX771905 Sequence
c	5	2848	97.6	337200	1	AP005280	AP005280 Corynebac
c	6	2848	97.6	349980	6	AX127150	AX127150 Sequence
c	7	2247	77.0	306650	1	AP005221	AP005221 Corynebac
c	8	1676	57.4	348408	1	BX248358	BX248358 Corynebac
c	9	1206.5	41.3	37586	6	AX191745	AX191745 Sequence
c	10	1206.5	41.3	306050	1	BX248341	BX248341 Mycobacte
c	11	1206.5	41.3	348247	15	BX842579	Bx842579 Mycobacte
c	12	1203	41.2	38859	1	MLCB268	AL022602 Mycobacte
	13	1203	41.2	348450	1	MLEPRTN4	AL583920 Mycobacte
c	14	1201.5	41.2	15776	1	AE007069	AE007069 Mycobacte
	15	626	21.5	2951	1	AF123319	AF123319 Streptomy
c	16	626	21.5	321250	1	SCO939111	AL939111 Streptomy

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2004, 09:57:30 ; Search time 516.558 Seconds
(without alignments)
4778.171 Million cell updates/sec

Title: US-09-623-596-2
Perfect score: 2918
Sequence: 1 MVTRIALVIAGVLIIRLGWV.....TRNTGLPSRVLHPLMILDLL 581

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09623596/runat_09092004_094652_11690/app_query.fasta_1
.1486

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09623596_@CGN_1_1_886_@runat_09092004_094652_11690 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2918	100.0	5347	2	AAZ09633	Aaz09633 B. lactof
	2	2848	97.6	1953	5	AAH67337	Aah67337 C glutami
	3	2848	97.6	2242	9	ADD13716	Add13716 C. glutam
c	4	2848	97.6	349980	5	AAH68531	Aah68531 C glutami
	5	1674	57.4	1827	7	ACA29976	Aca29976 Prokaryot
	6	1206.5	41.3	2040	4	AAH52030	Aah52030 Mycobacte
	7	1206.5	41.3	2040	7	ACA40605	Aca40605 Prokaryot
c	8	1206.5	41.3	110000	4	AAI99682_24	Continuation (25 o
	9	1203	41.2	2028	7	ACA39728	Aca39728 Prokaryot
c	10	1201.5	41.2	110000	4	AAI99683_24	Continuation (25 o
	11	1199	41.1	1989	7	ACA38015	Aca38015 Prokaryot
	12	1179.5	40.4	1937	7	ACA38413	Aca38413 Prokaryot
	13	604	20.7	349980	6	ABQ81848	Abq81848 Bifidobac
	14	580	19.9	12131	4	AAS59572	Aas59572 Propionib
	15	580	19.9	12131	7	ACF64501	Acf64501 Propionib
c	16	526.5	18.0	110000	6	ABQ69245_21	Continuation (22 o
	17	526.5	18.0	213251	6	ABQ67193	Abq67193 Listeria
	18	520	17.8	2178	7	ACA28148	Aca28148 Prokaryot
	19	514.5	17.6	1977	7	ACA29543	Aca29543 Prokaryot
	20	496	17.0	1740	7	ACA42602	Aca42602 Prokaryot
	21	494.5	16.9	2256	7	ACA36564	Aca36564 Prokaryot
c	22	494.5	16.9	110000	6	ABA03041_21	Continuation (22 o
	23	491	16.8	1764	7	ACA53863	Aca53863 Prokaryot
	24	484.5	16.6	1818	7	ACA27874	Aca27874 Prokaryot
	25	474	16.2	1767	7	ACF71678	Acf71678 Photorhab
	26	474	16.2	110000	7	ACF67367_48	Continuation (49 o
	27	474	16.2	110000	7	ACF65387_0	Acf65387 Photorhab
	28	472.5	16.2	1764	7	ACA35526	Aca35526 Prokaryot
	29	465.5	16.0	1746	7	ACA44262	Aca44262 Prokaryot
	30	465	15.9	2298	8	ADB11843	Adb11843 Alloiococ
	31	465	15.9	2298	8	ADB11845	Adb11845 Alloiococ
c	32	465	15.9	110000	8	ADB12064_13	Continuation (14 o
	33	460	15.8	1743	7	ACA53408	Aca53408 Prokaryot
	34	459.5	15.7	1728	7	ACA45661	Aca45661 Prokaryot
	35	457.5	15.7	2226	4	AAS51352	Aas51352 Enterococ
	36	457.5	15.7	2229	4	AAS52900	Aas52900 Enterococ
	37	457	15.7	2226	7	ACA18435	Aca18435 Prokaryot
	38	454	15.6	1714	7	ACA31790	Aca31790 Prokaryot
	39	453.5	15.5	1767	4	AAS52291	Aas52291 E. coli D
	40	453.5	15.5	1767	5	AAH81456	Aah81456 Escherich
	41	453.5	15.5	1767	7	ACA32355	Aca32355 Prokaryot
	42	453.5	15.5	1767	7	ACA51127	Aca51127 Prokaryot
	43	449.5	15.4	1750	7	ACA49176	Aca49176 Prokaryot
	44	449.5	15.4	1845	7	ACA23990	Aca23990 Prokaryot
	45	444.5	15.2	1746	4	AAS56356	Aas56356 Salmonell

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2004, 14:39:16 ; Search time 3286.03 Seconds
(without alignments)
5279.912 Million cell updates/sec

Title: US-09-623-596-2
Perfect score: 2918
Sequence: 1 MVTRIALVIAGVLIIRLGWV.....TRNTGLPSRVLHPLMILDLL 581

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09623596/runat_09092004_094653_11712/app_query.fasta_1
.1486

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09623596@CGN_1_1_6628@runat_09092004_094653_11712 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*

11: gb_htc:*
 12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	342	11.7	507	28	BH740525		BH740525	cpbav0010
	2	244	8.4	6303	28	BH771012		BH771012	LLMGtag73
	3	237	8.1	1344	28	BH770683		BH770683	LLMGtag43
	4	227	7.8	1133	28	BZ565848		BZ565848	pacs2-164
	5	220	7.5	1297	28	BZ565839		BZ565839	pacs2-164
	6	219	7.5	1138	28	BZ568217		BZ568217	pacs2-164
	7	214.5	7.4	1469	28	BZ572326		BZ572326	msh2_2585
c	8	209	7.2	962	28	BZ554173		BZ554173	pacs1-60_
c	9	204	7.0	812	29	CNS0104Q		AL153067	Anopheles
	10	190	6.5	785	28	BH795496		BH795496	30B12LLI0
c	11	189.5	6.5	713	14	CF887190		CF887190	UI-CF-FN0
	12	178.5	6.1	930	28	AF036000		AF036000	AF036000
c	13	177.5	6.1	609	28	CC063491		CC063491	fgma001d0
c	14	176	6.0	1060	28	AF095377		AF095377	AF095377
	15	168	5.8	958	28	AF029629		AF029629	AF029629
	16	163	5.6	826	28	BZ571950		BZ571950	msh2_216.
	17	154.5	5.3	307	10	BF065979		BF065979	HV_CEb001
c	18	152	5.2	1401	28	BZ552366		BZ552366	pacs1-60_
c	19	148	5.1	528	14	CF324573		CF324573	HDN--06-O
c	20	146.5	5.0	1342	28	BZ553468		BZ553468	pacs1-60_
c	21	137.5	4.7	1113	28	BZ558395		BZ558395	pacs1-60_
c	22	137.5	4.7	1600	28	BH770611		BH770611	LLMGtag37
	23	137	4.7	1030	28	BZ562490		BZ562490	pacs2-164
	24	133.5	4.6	966	12	BG676279		BG676279	602622680
	25	133	4.6	1161	28	BZ567531		BZ567531	pacs2-164
	26	131	4.5	2396	11	AK029491		AK029491	Mus muscu
c	27	129.5	4.4	1002	28	BZ576640		BZ576640	msh2_5032
	28	127.5	4.4	3664	29	AY407030		AY407030	Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 17:46:11 ; Search time 204 Seconds
(without alignments)
7135.472 Million cell updates/sec

Title: US-09-623-596-1_COPY_1_2623
Perfect score: 2623
Sequence: 1 aagcttcggggaggggcgcg.....tgatgatcctcgatttg 2623

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result	Query							
No.	Score	Match	Length	DB	ID	Description		
c	1	390	14.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli	
c	2	390	14.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
	3	71.6	2.7	1782	4	US-09-252-991A-8703	Sequence 8703, Ap	
	4	71.6	2.7	1830	4	US-09-252-991A-8916	Sequence 8916, Ap	
	5	63.8	2.4	1815	4	US-09-252-991A-7621	Sequence 7621, Ap	
c	6	63.8	2.4	1932	4	US-09-252-991A-7931	Sequence 7931, Ap	
c	7	56.4	2.2	960	4	US-09-252-991A-9077	Sequence 9077, Ap	
	8	51.2	2.0	2232	4	US-09-134-000C-1279	Sequence 1279, Ap	
c	9	50	1.9	7218	1	US-08-232-463-14	Sequence 14, Appl	
	10	45.8	1.7	1764	4	US-09-489-039A-5156	Sequence 5156, Ap	
	11	44	1.7	1812	4	US-09-543-681A-2803	Sequence 2803, Ap	

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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 20:46:57 ; Search time 1188 Seconds
(without alignments)
11109.162 Million cell updates/sec

Title: US-09-623-596-1_COPY_1_2623
Perfect score: 2623
Sequence: 1 aagcttcggggaggggcgcg.....tgatgatcctcgatttggtg 2623

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			% Query				ID	Description
	No.	Score	Match	Length	DB			
c	1	2511.6	95.8	3309400	9	US-09-738-626-1	Sequence 1, Appli	
	2	1758.6	67.0	1953	9	US-09-738-626-2372	Sequence 2372, Ap	
	3	596.6	22.7	1827	13	US-10-282-122A-17846	Sequence 17846, A	
	4	595	22.7	795	9	US-09-738-626-2373	Sequence 2373, Ap	
	5	403.2	15.4	1989	13	US-10-282-122A-25885	Sequence 25885, A	
	6	399	15.2	2028	13	US-10-282-122A-27598	Sequence 27598, A	
	7	390	14.9	2040	9	US-09-712-363-84	Sequence 84, Appl	
	8	390	14.9	2040	13	US-10-282-122A-28475	Sequence 28475, A	
	9	379.6	14.5	1937	13	US-10-282-122A-26283	Sequence 26283, A	
	10	155	5.9	2256646	17	US-10-470-565-1	Sequence 1, Appli	
	11	101.6	3.9	1959	15	US-10-156-761-6093	Sequence 6093, Ap	
	12	101.6	3.9	9025608	15	US-10-156-761-1	Sequence 1, Appli	
	13	84.8	3.2	2178	13	US-10-282-122A-16018	Sequence 16018, A	
	14	83.8	3.2	1818	13	US-10-282-122A-15744	Sequence 15744, A	
	15	82.6	3.1	1746	13	US-10-282-122A-32132	Sequence 32132, A	
	16	73.6	2.8	2731748	17	US-10-297-465A-1	Sequence 1, Appli	
	17	72.2	2.8	1842	13	US-10-282-122A-14100	Sequence 14100, A	
	18	71.8	2.7	1919	9	US-09-974-300-1666	Sequence 1666, Ap	
	19	70	2.7	1698	9	US-09-815-242-7770	Sequence 7770, Ap	
	20	70	2.7	1698	13	US-10-282-122A-30183	Sequence 30183, A	
	21	69.2	2.6	1845	13	US-10-282-122A-11860	Sequence 11860, A	
	22	67.4	2.6	2190	13	US-10-282-122A-15800	Sequence 15800, A	
	23	64	2.4	1863	13	US-10-282-122A-12918	Sequence 12918, A	
	24	63.8	2.4	1740	13	US-10-282-122A-30472	Sequence 30472, A	
	25	62.8	2.4	1716	13	US-10-282-122A-29337	Sequence 29337, A	
	26	59.2	2.3	1746	13	US-10-282-122A-29883	Sequence 29883, A	
	27	58.4	2.2	1719	13	US-10-282-122A-15195	Sequence 15195, A	
	28	56.6	2.2	1728	13	US-10-282-122A-33531	Sequence 33531, A	
	29	53.2	2.0	1959	13	US-10-282-122A-40409	Sequence 40409, A	
	30	51.6	2.0	1767	13	US-10-282-122A-38997	Sequence 38997, A	
	31	51.4	2.0	2247	13	US-10-282-122A-36335	Sequence 36335, A	
	32	51.2	2.0	2226	9	US-09-815-242-3934	Sequence 3934, Ap	
	33	51.2	2.0	2226	13	US-10-282-122A-6305	Sequence 6305, Ap	
	34	51.2	2.0	2229	9	US-09-815-242-6537	Sequence 6537, Ap	
	35	51	1.9	1764	13	US-10-282-122A-41733	Sequence 41733, A	
	36	49.8	1.9	1750	13	US-10-282-122A-37046	Sequence 37046, A	
	37	49.4	1.9	1767	9	US-09-741-669-255	Sequence 255, App	
	38	49.4	1.9	1767	9	US-09-815-242-5928	Sequence 5928, Ap	
	39	49.4	1.9	1767	13	US-10-282-122A-20225	Sequence 20225, A	
	40	48.4	1.8	1714	13	US-10-282-122A-19660	Sequence 19660, A	
	41	47.2	1.8	2256	13	US-10-282-122A-38496	Sequence 38496, A	
	42	46.4	1.8	2256	13	US-10-282-122A-24434	Sequence 24434, A	
	43	46	1.8	1743	13	US-10-282-122A-41278	Sequence 41278, A	
	44	45.8	1.7	1764	13	US-10-282-122A-23396	Sequence 23396, A	
	45	44.8	1.7	1068	9	US-09-974-300-6191	Sequence 6191, Ap	

ALIGNMENTS

RESULT 1

US-09-738-626-1/c